Sequence Listing

<110> Botstein,David
   Desnoyers,Luc
   Ferrara,Napoleone
   Fong,Sherman
   Gao,Wei-Qiang
   Goddard,Audrey
   Gurney,Austin L.
   Pan,James
   Roy,Margaret Ann
   Stewart,Timothy A.
   Tumas,Daniel
   Watanabe,Colin K.
   Wood,William I.

<120> Secreted and Transmembrane Polypeptides and Nucleic
   Acids Encoding the Same

<130> P2930R1C6

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cgggatgacc cgccgggacc cgctcgcaaa taaggtggcc ctggtaacgg 150

cctccaccga cgggatcggc ttcgccatcg cccggcgttt ggcccaggac 200

ggggcccatg tggtcgtcag cagccggaag cagcagaatg tggaccaggc 250

ggtggccacg ctgcagggg aggggctgag cgtgacgggc accgtgtgcc 300

atgtggggaa ggcggaggac cgggagcggc tggtggccac ggctgtgaag 350

2

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acattaatgt gaaggcccca gccctgatga caaaggcagt ggtgccagaa 500

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gctctggatg gacaaggaaa aagaggaaag catgaaagaa accctgcgga 750

taagaaggtt aggcgagcca gaggattgtg ctggcatcgt gtctttcctg 800

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                 20                  25                  30

Ala Asn Lys Val Ala Leu Val Thr Ala Ser Thr Asp Gly Ile Gly
                 35                  40                  45

Phe Ala Ile Ala Arg Arg Leu Ala Gln Asp Gly Ala His Val Val
                 50                  55                  60

Val Ser Ser Arg Lys Gln Gln Asn Val Asp Gln Ala Val Ala Thr
                 65                  70                  75
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Leu Gln Gly Glu Gly Leu Ser Val Thr Gly Thr Val Cys His Val
                80   85   90

Gly Lys Ala Glu Asp Arg Glu Arg Leu Val Ala Thr Ala Val Lys
                95   100   105

Leu His Gly Gly Ile Asp Ile Leu Val Ser Asn Ala Ala Val Asn
               110   115   120

Pro Phe Phe Gly Ser Ile Met Asp Val Thr Glu Glu Val Trp Asp
               125   130   135

Lys Thr Leu Asp Ile Asn Val Lys Ala Pro Ala Leu Met Thr Lys
               140   145   150

Ala Val Val Pro Glu Met Glu Lys Arg Gly Gly Gly Ser Val Val
               155   160   165

Ile Val Ser Ser Ile Ala Ala Phe Ser Pro Ser Pro Gly Phe Ser
               170   175   180

Pro Tyr Asn Val Ser Lys Thr Ala Leu Leu Gly Leu Thr Lys Thr
               185   190   195

Leu Ala Ile Glu Leu Ala Pro Arg Asn Ile Arg Val Asn Cys Leu
               200   205   210

Ala Pro Gly Leu Ile Lys Thr Ser Phe Ser Arg Met Leu Trp Met
               215   220   225

Asp Lys Glu Lys Glu Glu Ser Met Lys Glu Thr Leu Arg Ile Arg
               230   235   240

Arg Leu Gly Glu Pro Glu Asp Cys Ala Gly Ile Val Ser Phe Leu
               245   250   255

Cys Ser Glu Asp Ala Ser Tyr Ile Thr Gly Glu Thr Val Val Val
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Gly Gly Gly Thr Pro Ser Arg Leu
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<210> 4
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<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

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<212> DNA
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 agaaccgaga ctttctggct gcgctggagg acgccatgga gcagtacaaa 200

 ctgcagagcg accggctgcg tgagcagcag gaggagatgg tggaactgcg 250

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 ggccctgaac cgccagcaca gccagcgtat ccgggagctg gagcaggagg 900
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5

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aagcgactgc aggagctcga gcggaacgtg cagctcatgc ggcagcagca 1150

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tggaacagca gcagaagatt gaggagcaga agaagtggct ggaccaggag 1400

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agaagacggg gctggagagc aagcgcctga gatccagcca ggccctcaac 1550

gaggacatcg tgcgagtgtc cagccggctg gagcacctgg agaaggagct 1600

gtccgagaag agcgggcagc tgcggcaggg cagcgcccag agccagcagc 1650

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ggccaagctc agctacctct catcctcaga gaccagagcc ctcctctgca 1950

agtattttga caaggtggtg acgctccgag aggagcagca ccagcagcag 2000

attgccttct cggaactgga gatgcagctg gaggagcagc agaggctggt 2050

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agctgaccct gcagcagaag gagcacgagc agaacatgca gctgctcctg 2150

cagcagagtc gagaccacct cggtgaaggg ttagcagaca gcaggaggca 2200

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cacagcaggg gtggggagaa gaggagcctg tgctcggagg gcagacaggc 2350
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6

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<210> 7
<211> 830
<212> PRT
<213> Homo sapiens

<400> 7

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                20                  25                  30

Gly Trp Gly Gly Leu Arg Leu Leu Asn Gly Leu Pro Pro Gly Ser
                35                  40                  45

Phe Val Pro Arg Pro His Thr Ala Pro Leu Gly Gly Ala His Ala
                50                  55                  60

His Val Leu Gly Met Val Pro Pro Ala Cys Leu Pro Gly Asp Glu
                65                  70                  75

Val Gly Ser Glu Gln Arg Gly Glu Gln Val Thr Asn Gly Arg Glu
                80                  85                  90

Ala Gly Ala Glu Leu Leu Thr Glu Val Asn Arg Leu Gly Ser Gly
                95                  100                 105
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7

Ser Ser Ala Ala Ser Glu Glu Glu Glu Glu Glu Glu Pro Pro
                110   115   120

Arg Arg Thr Leu His Leu Arg Arg Asn Arg Ile Ser Asn Cys Ser
                125   130   135

Gln Arg Ala Gly Ala Arg Pro Gly Ser Leu Pro Glu Arg Lys Gly
                140   145   150

Pro Glu Leu Cys Leu Glu Glu Leu Asp Ala Ala Ile Pro Gly Ser
                155   160   165

Arg Ala Val Gly Gly Ser Lys Ala Arg Val Gln Ala Arg Gln Val
                170   175   180

Pro Pro Ala Thr Ala Ser Glu Trp Arg Leu Ala Gln Ala Gln Gln
                185   190   195

Lys Ile Arg Glu Leu Ala Ile Asn Ile Arg Met Lys Glu Glu Leu
                200   205   210

Ile Gly Glu Leu Val Arg Thr Gly Lys Ala Ala Gln Ala Leu Asn
                215   220   225

Arg Gln His Ser Gln Arg Ile Arg Glu Leu Glu Gln Glu Ala Glu
                230   235   240

Gln Val Arg Ala Glu Leu Ser Glu Gly Gln Arg Gln Leu Arg Glu
                245   250   255

Leu Glu Gly Lys Glu Leu Gln Asp Ala Gly Glu Arg Ser Arg Leu
                260   265   270

Gln Glu Phe Arg Arg Arg Val Ala Ala Ala Gln Ser Gln Val Gln
                275   280   285

Val Leu Lys Glu Lys Lys Gln Ala Thr Glu Arg Leu Val Ser Leu
                290   295   300

Ser Ala Gln Ser Glu Lys Arg Leu Gln Glu Leu Glu Arg Asn Val
                305   310   315

Gln Leu Met Arg Gln Gln Gly Gln Leu Gln Arg Arg Leu Arg
                320   325   330

Glu Glu Thr Glu Gln Lys Arg Arg Leu Glu Ala Glu Met Ser Lys
                335   340   345

Arg Gln His Arg Val Lys Glu Leu Glu Leu Lys His Glu Gln Gln
                350   355   360

Gln Lys Ile Leu Lys Ile Lys Thr Glu Glu Ile Ala Ala Phe Gln
                365   370   375

Arg Lys Arg Arg Ser Gly Ser Asn Gly Ser Val Val Ser Leu Glu
                380   385   390

Gln Gln Gln Lys Ile Glu Glu Gln Lys Lys Trp Leu Asp Gln Glu

8

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     Glu Glu Leu His Lys Arg Glu Ala Ile Leu Ala Lys Lys Glu Ala
                         425                    430                    435
     Leu Met Gln Glu Lys Thr Gly Leu Glu Ser Lys Arg Leu Arg Ser
                         440                    445                    450
     Ser Gln Ala Leu Asn Glu Asp Ile Val Arg Val Ser Ser Arg Leu
                         455                    460                    465
     Glu His Leu Glu Lys Glu Leu Ser Glu Lys Ser Gly Gln Leu Arg
                         470                    475                    480
     Gln Gly Ser Ala Gln Ser Gln Gln Gln Ile Arg Gly Glu Ile Asp
                         485                    490                    495
     Ser Leu Arg Gln Glu Lys Asp Ser Leu Leu Lys Gln Arg Leu Glu
                         500                    505                    510
     Ile Asp Gly Lys Leu Arg Gln Gly Ser Leu Leu Ser Pro Glu Glu
                         515                    520                    525
     Glu Arg Thr Leu Phe Gln Leu Asp Glu Ala Ile Glu Ala Leu Asp
                         530                    535                    540
     Ala Ala Ile Glu Tyr Lys Asn Glu Ala Ile Thr Cys Arg Gln Arg
                         545                    550                    555
     Val Leu Arg Ala Ser Ala Ser Leu Leu Ser Gln Cys Glu Met Asn
                         560                    565                    570
     Leu Met Ala Lys Leu Ser Tyr Leu Ser Ser Ser Glu Thr Arg Ala
                         575                    580                    585
     Leu Leu Cys Lys Tyr Phe Asp Lys Val Val Thr Leu Arg Glu Glu
                         590                    595                    600
     Gln His Gln Gln Gln Ile Ala Phe Ser Glu Leu Glu Met Gln Leu
                         605                    610                    615
     Glu Glu Gln Gln Arg Leu Val Tyr Trp Leu Glu Val Ala Leu Glu
                         620                    625                    630
     Arg Gln Arg Leu Glu Met Asp Arg Gln Leu Thr Leu Gln Gln Lys
                         635                    640                    645
     Glu His Glu Gln Asn Met Gln Leu Leu Leu Gln Gln Ser Arg Asp
                         650                    655                    660
     His Leu Gly Glu Gly Leu Ala Asp Ser Arg Arg Gln Tyr Glu Ala
                         665                    670                    675
     Arg Ile Gln Ala Leu Glu Lys Glu Leu Gly Arg Tyr Met Trp Ile
                         680                    685                    690
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9

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Asn Gln Glu Leu Lys Gln Lys Leu Gly Gly Val Asn Ala Val Gly
              695             700                 705

His Ser Arg Gly Gly Glu Lys Arg Ser Leu Cys Ser Glu Gly Arg
              710             715                 720

Gln Ala Pro Gly Asn Glu Asp Glu Leu His Leu Ala Pro Glu Leu
              725             730                 735

Leu Trp Leu Ser Pro Leu Thr Glu Gly Ala Pro Arg Thr Arg Glu
              740             745                 750

Glu Thr Arg Asp Leu Val His Ala Pro Leu Pro Leu Thr Trp Lys
              755             760                 765

Arg Ser Ser Leu Cys Gly Glu Glu Gln Gly Ser Pro Glu Glu Leu
              770             775                 780

Arg Gln Arg Glu Ala Ala Glu Pro Leu Val Gly Arg Val Leu Pro
              785             790                 795

Val Gly Glu Ala Gly Leu Pro Trp Asn Phe Gly Pro Leu Ser Lys
              800             805                 810

Pro Arg Arg Glu Leu Arg Arg Ala Ser Pro Gly Met Ile Asp Val
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Arg Lys Asn Pro Leu
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<210> 8
<211> 662
<212> DNA
<213> Homo sapiens

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acagacgctc ctgttggctc aggactgtgg ctgtgccagc cgacacccag 150

gtgtgggaac aagatctaca acccttcaga gcagtgctgt tatgatgatg 200

ccatcttatc cttaaaggag acccgccgct gtggctccac ctgcaccttc 250

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gtttcttgtg aagttgaggg ttctgggtat gaagtctcag tgtcacttat 350

ctcccatctc ccggagctgt accaggaaca ggaggcacgt cctgtaccca 400

taaaaacccc aggctccact ggcagacggc agacaagggg agaagagacg 450

aagcagctgg acatcggaga ctacagttga acttcggaga gaagcaactt 500

gacttcagag ggatggctca atgacatagc tttggagagg agcccagctg 550
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10

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gggatggcca gacttcaggg gaagaatgcc ttcctgcttc atcccctttc 600

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catttaccat ct 662
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<212> PRT
<213> Homo sapiens

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                    20                  25                  30

  Gly Ser Gly Leu Trp Leu Cys Gln Pro Thr Pro Arg Cys Gly Asn
                    35                  40                  45

  Lys Ile Tyr Asn Pro Ser Glu Gln Cys Cys Tyr Asp Asp Ala Ile
                    50                  55                  60

  Leu Ser Leu Lys Glu Thr Arg Arg Cys Gly Ser Thr Cys Thr Phe
                    65                  70                  75

  Trp Pro Cys Phe Glu Leu Cys Cys Pro Glu Ser Phe Gly Pro Gln
                    80                  85                  90

  Gln Lys Phe Leu Val Lys Leu Arg Val Leu Gly Met Lys Ser Gln
                    95                  100                 105

  Cys His Leu Ser Pro Ile Ser Arg Ser Cys Thr Arg Asn Arg Arg
                    110                 115                 120

  His Val Leu Tyr Pro
                    125
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<210> 10
<211> 1942
<212> DNA
<213> Homo sapiens

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 ctgccgggtc tggagagctc cccgaacccc tccgcggaga ggagcgaggc 150

 ggcgccaggg tggcccccgg ggcgcgcttg gtctcggaga agcggggacg 200

 aggccggagg atgagcgact gagggcgacg cgggcactga cgcgagttgg 250

 ggccgcgact accggcagct gacagcgcga tgagcgactc cccagagacg 300

 ccctagcccg gtgtgcgcgc caggcggagc gcgcaggtgg ggctgggctg 350
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11

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ttagtggtcc gccccacgcg ggtcgccggc cggcccagga tgggcgctgg 400

caacccgggc gcgcgcccgc cgctgctacc cctgcgcccg ctgcgagccc 450

ggcgtccggc ccgcgccctg cgctcatgga cggcggctcc cggctggcgg 500

cggcgcgccc ccgggctgtg aatgcgactc gcccctcggc cgcgctcccc 550

gcccgcccgc ccgccgggac gtggtagggg atgcccagct ccactgcgat 600

ggcagttggc gcgctctcca gttccctcct ggtcacctgc tgcctgatgg 650

tggctctgtg cagtccgagc atcccgctgg agaagctggc ccaggcacca 700

gagcagccgg gccaggagaa gcgtgagcac gccactcggg acggcccggg 750

gcgggtgaac gagctcgggc gcccggcgag ggacgagggc ggcagcggcc 800

gggactggaa gagcaagagc ggccgtgggc tcgccggccg tgagccgtgg 850

agcaagctga agcaggcctg ggtctcccag ggcggggggcg ccaaggccgg 900

ggatctgcag gtccggcccc gcggggacac cccgcaggcg gaagccctgg 950

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ccacccgagg agtacgtgta cccggactac cgtggcaagg gctgcgtgga 1050

cgagagcggc ttcgtgtacg cgatcgggga gaagttcgcg ccgggccct 1100

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tactgatgtg aacattctag atgactctgg gaactatcag tcaaagaaga 1650

cttttgatga ggaataatgg aaaattgttg gtacttttcc ttttcttgat 1700

aacagttact acaacagaag gaaatggata tatttcaaaa catcaacaag 1750

aactttgggc ataaaatcct tctctaaata aatgtgctat tttcacagta 1800
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12

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agtacacaaa agtacactat tatatatcaa atgtatttct ataatccctc 1850

cattagagag cttatataag tgttttctat agatgcagat taaaaatgct 1900

gtgttgtcaa ccgtcaaaaa aaaaaaaaaa aaaaaaaaaa aa 1942
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<210> 11
<211> 325
<212> PRT
<213> Homo sapiens

<400> 11

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Leu Leu Val Thr Cys Cys Leu Met Val Ala Leu Cys Ser Pro Ser
                20                  25                  30

Ile Pro Leu Glu Lys Leu Ala Gln Ala Pro Glu Gln Pro Gly Gln
                35                  40                  45

Glu Lys Arg Glu His Ala Thr Arg Asp Gly Pro Gly Arg Val Asn
                50                  55                  60

Glu Leu Gly Arg Pro Ala Arg Asp Glu Gly Gly Ser Gly Arg Asp
                65                  70                  75

Trp Lys Ser Lys Ser Gly Arg Gly Leu Ala Gly Arg Glu Pro Trp
                80                  85                  90

Ser Lys Leu Lys Gln Ala Trp Val Ser Gln Gly Gly Gly Ala Lys
                95                  100                 105

Ala Gly Asp Leu Gln Val Arg Pro Arg Gly Asp Thr Pro Gln Ala
                110                 115                 120

Glu Ala Leu Ala Ala Ala Ala Gln Asp Ala Ile Gly Pro Glu Leu
                125                 130                 135

Ala Pro Thr Pro Glu Pro Pro Glu Glu Tyr Val Tyr Pro Asp Tyr
                140                 145                 150

Arg Gly Lys Gly Cys Val Asp Glu Ser Gly Phe Val Tyr Ala Ile
                155                 160                 165

Gly Glu Lys Phe Ala Pro Gly Pro Ser Ala Cys Pro Cys Leu Cys
                170                 175                 180

Thr Glu Glu Gly Pro Leu Cys Ala Gln Pro Glu Cys Pro Arg Leu
                185                 190                 195

His Pro Arg Cys Ile His Val Asp Thr Ser Gln Cys Cys Pro Gln
                200                 205                 210

Cys Lys Glu Arg Lys Asn Tyr Cys Glu Phe Arg Gly Lys Thr Tyr
                215                 220                 225

Gln Thr Leu Glu Glu Phe Val Val Ser Pro Cys Glu Arg Cys Arg
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13

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                230                      235                      240
   Cys Glu Ala Asn Gly Glu Val Leu Cys Thr Val Ser Ala Cys Pro
                    245                  250                  255

   Gln Thr Glu Cys Val Asp Pro Val Tyr Glu Pro Asp Gln Cys Cys
                    260                  265                  270

   Pro Ile Cys Lys Asn Gly Pro Asn Cys Phe Ala Glu Thr Ala Val
                    275                  280                  285

   Ile Pro Ala Gly Arg Glu Val Lys Thr Asp Glu Cys Thr Ile Cys
                    290                  295                  300

   His Cys Thr Tyr Glu Glu Gly Thr Trp Arg Ile Glu Arg Gln Ala
                    305                  310                  315

   Met Cys Thr Arg His Glu Cys Arg Gln Met
                    320                  325
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<210> 12
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 12
 gaggtgtcgc tgtgaagcca acgg 24

<210> 13
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 13
 cgctcgattc tccatgtgcc ttcc 24

<210> 14
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 14
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<210> 15
<211> 1587
<212> DNA
<213> Homo sapiens

<400> 15
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gttcagcatg tgtggaaggt gtccgaccta ccccggcaat ggacccctaa 150

gaacaccagc tgcgacagcg gcttggggtg ccaggacacg ttgatgctca 200

ttgagagcgg accccaagtg agcctggtgc tctccaaggg ctgcacggag 250

gccaaggacc aggagccccg cgtcactgag caccggatgg ccccggcct 300

ctccctgatc tcctacacct tcgtgtgccg ccaggaggac ttctgcaaca 350

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tcctcaggct caggggagga ggcatcttct ccaatctgag agtccaggga 550

tgcatgcccc agccaggttg caacctgctc aatgggacac aggaaattgg 600

gcccgtgggt atgactgaga actgcaatag gaaagatttt ctgacctgtc 650

atcgggggac caccattatg acacacggaa acttggctca agaacccact 700

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ttcaccgctg ctgaccaccc acactcaacc tccctctgac ctcataacct 1400

aatggccttg gacaccagat tctttcccat tctgtccatg aatcatcttc 1450

15

cccacacaca atcattcata tctactcacc taacagcaac actggggaga 1500

gcctggagca tccggacttg ccctatggga gaggggacgc tggaggagtg 1550

gctgcatgta tctgataata cagaccctgt cctttca 1587

<210> 16
<211> 437
<212> PRT
<213> Homo sapiens

<400> 16
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Met Ser Ala Val Leu Leu Leu Ala Leu Leu Gly Phe Ile Leu Pro
 1               5                  10                  15

Leu Pro Gly Val Gln Ala Leu Leu Cys Gln Phe Gly Thr Val Gln
                 20                  25                  30

His Val Trp Lys Val Ser Asp Leu Pro Arg Gln Trp Thr Pro Lys
                 35                  40                  45

Asn Thr Ser Cys Asp Ser Gly Leu Gly Cys Gln Asp Thr Leu Met
                 50                  55                  60

Leu Ile Glu Ser Gly Pro Gln Val Ser Leu Val Leu Ser Lys Gly
                 65                  70                  75

Cys Thr Glu Ala Lys Asp Gln Glu Pro Arg Val Thr Glu His Arg
                 80                  85                  90

Met Gly Pro Gly Leu Ser Leu Ile Ser Tyr Thr Phe Val Cys Arg
                 95                  100                 105

Gln Glu Asp Phe Cys Asn Asn Leu Val Asn Ser Leu Pro Leu Trp
                 110                 115                 120

Ala Pro Gln Pro Pro Ala Asp Pro Gly Ser Leu Arg Cys Pro Val
                 125                 130                 135

Cys Leu Ser Met Glu Gly Cys Leu Glu Gly Thr Thr Glu Glu Ile
                 140                 145                 150

Cys Pro Lys Gly Thr Thr His Cys Tyr Asp Gly Leu Leu Arg Leu
                 155                 160                 165

Arg Gly Gly Gly Ile Phe Ser Asn Leu Arg Val Gln Gly Cys Met
                 170                 175                 180

Pro Gln Pro Gly Cys Asn Leu Leu Asn Gly Thr Gln Glu Ile Gly
                 185                 190                 195

Pro Val Gly Met Thr Glu Asn Cys Asn Arg Lys Asp Phe Leu Thr
                 200                 205                 210

Cys His Arg Gly Thr Thr Ile Met Thr His Gly Asn Leu Ala Gln
                 215                 220                 225

Glu Pro Thr Asp Trp Thr Thr Ser Asn Thr Glu Met Cys Glu Val
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16

Gly Gln Val Cys Gln Glu Thr Leu Leu Leu Ile Asp Val Gly Leu
                    245   250   255

Thr Ser Thr Leu Val Gly Thr Lys Gly Cys Ser Thr Val Gly Ala
                    260   265   270

Gln Asn Ser Gln Lys Thr Thr Ile His Ser Ala Pro Pro Gly Val
                    275   280   285

Leu Val Ala Ser Tyr Thr His Phe Cys Ser Ser Asp Leu Cys Asn
                    290   295   300

Ser Ala Ser Ser Ser Ser Val Leu Leu Asn Ser Leu Pro Pro Gln
                    305   310   315

Ala Ala Pro Val Pro Gly Asp Arg Gln Cys Pro Thr Cys Val Gln
                    320   325   330

Pro Leu Gly Thr Cys Ser Ser Gly Ser Pro Arg Met Thr Cys Pro
                    335   340   345

Arg Gly Ala Thr His Cys Tyr Asp Gly Tyr Ile His Leu Ser Gly
                    350   355   360

Gly Gly Leu Ser Thr Lys Met Ser Ile Gln Gly Cys Val Ala Gln
                    365   370   375

Pro Ser Ser Phe Leu Leu Asn His Thr Arg Gln Ile Gly Ile Phe
                    380   385   390

Ser Ala Arg Glu Lys Arg Asp Val Gln Pro Pro Ala Ser Gln His
                    395   400   405

Glu Gly Gly Gly Ala Glu Gly Leu Glu Ser Leu Thr Trp Gly Val
                    410   415   420

Gly Leu Ala Leu Ala Pro Ala Leu Trp Trp Gly Val Val Cys Pro
                    425   430   435

Ser Cys

<210> 17
<211> 2387
<212> DNA
<213> Homo sapiens

<400> 17
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 gccgcggccc tggctgcggc gctgctctcg tcgcttgcgc gctgctctct 100

 tctagagccg agggacccgg tggcctcgtc gctcagcccc tatttcggca 150

 ccaagactcg ctacgaggat gtcaaccccg tgctattgtc gggccccgag 200

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gctccgtggc gggaccctga gctgctggag gggacctgca ccccggtgca 250

gctggtcgcc gtcattcgcc acggcacccg ctaccccacg gtcaaacaga 300

tccgcaagct gaggcagctg cacgggttgc tgcaggcccg cgggtccagg 350

gatggcgggg ctagtagtac cggcagccgc gacctgggtg cagcgctggc 400

cgactggcct ttgtggtacg cggactggat ggacgggcag ctagtagaga 450

agggacggca ggatatgcga cagctggcgc tgcgtctggc ctcgctcttc 500

ccggcccttt tcagccgtga gaactacggc cgcctgcggc tcatcaccag 550

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tttggacctc caacagttaa tgataaacta atgagatttt ttgatcactg 700

tgagaagttt ttaactgaag tagaaaaaaa tgctacagct ctttatcacg 750

tggaagcctt caaaactgga ccagaaatgc agaacatttt aaaaaaagtt 800

gcagctactt tgcaagtgcc agtaaatgat ttaaatgcag atttaattca 850

agtagccttt ttcacctgtt catttgacct ggcaattaaa ggtgttaaat 900

ctccttggtg tgatgttttt gacatagatg atgcaaaggt attagaatat 950

ttaaatgatc tgaaacaata ttggaaaaga ggatatgggt atactattaa 1000

cagtcgatcc agctgcacct tgtttcagga tatctttcag cacttggaca 1050

aagcagttga acagaaacaa aggtctcagc caatttcttc tccagtcatc 1100

ctccagtttg gtcatgcaga gactcttctt ccactgcttt ctctcatggg 1150

ctacttcaaa gacaaggaac ccctaacagc gtacaattac aaaaaacaaa 1200

tgcatcggaa gttccgaagt ggtctcattg taccttatgc ctcgaacctg 1250

atatttgtgc tttaccactg tgaaaatgct aagactccta aagaacaatt 1300

ccgagtgcag atgttattaa atgaaaaggt gttacctttg gcttactcac 1350

aagaaactgt ttcattttat gaagatctga agaaccacta caaggacatc 1400

cttcagagtt gtcaaaccag tgaagaatgt gaattagcaa gggctaacag 1450

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attgggtttc tctctgggtt tggacatgaa atgtaagaaa agatttttca 1650
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18

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ctggagcagc tctcttaagg agaaacaaat ctatttagag aaacagctgg 1700

ccctgcaaat gtttacagaa atgaaattct tcctacttat ataagaaatc 1750

tcacactgag atagaattgt gatttcataa taacacttga aaagtgctgg 1800

agtaacaaaa tatctcagtt ggaccatcct taacttgatt gaactgtcta 1850

ggaactttac agattgttct gcagttctct cttctttttcc tcaggtagga 1900

cagctctagc attttcttaa tcaggaatat tgtggtaagc tgggagtatc 1950

actctggaag aaagtaacat ctccagatga gaatttgaaa caagaaacag 2000

agtgttgtaa aaggacacct tcactgaagc aagtcggaaa gtacaatgaa 2050

aataaatatt tttggtattt atttatgaaa tatttgaaca ttttttcaat 2100

aattcctttt tacttctagg aagtctcaaa agaccatctt aaattattat 2150

atgtttggac aattagcaac aagtcagata gttagaatcg aagtttttca 2200

aatccattgc ttagctaact ttttcattct gtcacttggc ttcgattttt 2250

atattttcct attatatgaa atgtatcttt tggttgtttg attttttcttt 2300

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ctataataaa gaaaattctt gtgactttaa aaaaaaa 2387
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<210> 18
<211> 487
<212> PRT
<213> Homo sapiens

<400> 18
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Met Leu Arg Ala Pro Gly Cys Leu Leu Arg Thr Ser Val Ala Pro
 1               5                  10                  15

Ala Ala Ala Leu Ala Ala Ala Leu Leu Ser Ser Leu Ala Arg Cys
                20                  25                  30

Ser Leu Leu Glu Pro Arg Asp Pro Val Ala Ser Ser Leu Ser Pro
    .           35                  40                  45

Tyr Phe Gly Thr Lys Thr Arg Tyr Glu Asp Val Asn Pro Val Leu
                50                  55                  60

Leu Ser Gly Pro Glu Ala Pro Trp Arg Asp Pro Glu Leu Leu Glu
                65                  70                  75

Gly Thr Cys Thr Pro Val Gln Leu Val Ala Leu Ile Arg His Gly
                80                  85                  90

Thr Arg Tyr Pro Thr Val Lys Gln Ile Arg Lys Leu Arg Gln Leu
                95                  100                 105

His Gly Leu Leu Gln Ala Arg Gly Ser Arg Asp Gly Gly Ala Ser
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```

19
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Ser Thr Gly Ser Arg Asp Leu Gly Ala Ala Leu Ala Asp Trp Pro
                125   130   135

Leu Trp Tyr Ala Asp Trp Met Asp Gly Gln Leu Val Glu Lys Gly
                140   145   150

Arg Gln Asp Met Arg Gln Leu Ala Leu Arg Leu Ala Ser Leu Phe
                155   160   165

Pro Ala Leu Phe Ser Arg Glu Asn Tyr Gly Arg Leu Arg Leu Ile
                170   175   180

Thr Ser Ser Lys His Arg Cys Met Asp Ser Ser Ala Ala Phe Leu
                185   190   195

Gln Gly Leu Trp Gln His Tyr His Pro Gly Leu Pro Pro Pro Asp
                200   205   210

Val Ala Asp Met Glu Phe Gly Pro Pro Thr Val Asn Asp Lys Leu
                215   220   225

Met Arg Phe Phe Asp His Cys Glu Lys Phe Leu Thr Glu Val Glu
                230   235   240

Lys Asn Ala Thr Ala Leu Tyr His Val Glu Ala Phe Lys Thr Gly
                245   250   255

Pro Glu Met Gln Asn Ile Leu Lys Lys Val Ala Ala Thr Leu Gln
                260   265   270

Val Pro Val Asn Asp Leu Asn Ala Asp Leu Ile Gln Val Ala Phe
                275   280   285

Phe Thr Cys Ser Phe Asp Leu Ala Ile Lys Gly Val Lys Ser Pro
                290   295   300

Trp Cys Asp Val Phe Asp Ile Asp Asp Ala Lys Val Leu Glu Tyr
                305   310   315

Leu Asn Asp Leu Lys Gln Tyr Trp Lys Arg Gly Tyr Gly Tyr Thr
                320   325   330

Ile Asn Ser Arg Ser Ser Cys Thr Leu Phe Gln Asp Ile Phe Gln
                335   340   345

His Leu Asp Lys Ala Val Glu Gln Lys Gln Arg Ser Gln Pro Ile
                350   355   360

Ser Ser Pro Val Ile Leu Gln Phe Gly His Ala Glu Thr Leu Leu
                365   370   375

Pro Leu Leu Ser Leu Met Gly Tyr Phe Lys Asp Lys Glu Pro Leu
                380   385   390

Thr Ala Tyr Asn Tyr Lys Lys Gln Met His Arg Lys Phe Arg Ser
                395   400   405

20

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Gly Leu Ile Val Pro Tyr Ala Ser Asn Leu Ile Phe Val Leu Tyr
                410                 415                 420

His Cys Glu Asn Ala Lys Thr Pro Lys Glu Gln Phe Arg Val Gln
                425                 430                 435

Met Leu Leu Asn Glu Lys Val Leu Pro Leu Ala Tyr Ser Gln Glu
                440                 445                 450

Thr Val Ser Phe Tyr Glu Asp Leu Lys Asn His Tyr Lys Asp Ile
                455                 460                 465

Leu Gln Ser Cys Gln Thr Ser Glu Glu Cys Glu Leu Ala Arg Ala
                470                 475                 480

Asn Ser Thr Ser Asp Glu Leu
                485
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<210> 19
<211> 3554
<212> DNA
<213> Homo sapiens

<400> 19

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gggactacaa gccgcgccgc gctgccgctg gcccctcagc aaccctcgac 50

atggcgctga ggcggccacc gcgactccgg ctctgcgctc ggctgcctga 100

cttcttcctg ctgctgcttt tcaggggctg cctgataggg gctgtaaatc 150

tcaaatccag caatcgaacc ccagtggtac aggaatttga aagtgtggaa 200

ctgtcttgca tcattacgga ttcgcagaca agtgacccca ggatcgagtg 250

gaagaaaatt caagatgaac aaaccacata tgtgtttttt gacaacaaaa 300

ttcagggaga cttggcgggt cgtgcagaaa tactggggaa gacatccctg 350

aagatctgga atgtgacacg gagagactca gccctttatc gctgtgaggt 400

cgttgctcga aatgaccgca aggaaattga tgagattgtg atcgagttaa 450

ctgtgcaagt gaagccagtg acccctgtct gtagagtgcc gaaggctgta 500

ccagtaggca agatggcaac actgcactgc caggagagtg agggccaccc 550

ccggcctcac tacagctggt atcgcaatga tgtaccactg cccacggatt 600

ccagagccaa tcccagattt cgcaattctt ctttccactt aaactctgaa 650

acaggcactt tggtgttcac tgctgttcac aaggacgact ctgggcagta 700

ctactgcatt gcttccaatg acgcaggctc agccaggtgt gaggagcagg 750

agatggaagt ctatgacctg aacattggcg gaattattgg ggggttctg 800

gttgtccttg ctgtactggc cctgatcacg ttgggcatct gctgtgcata 850
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cagacgtggc tacttcatca acaataaaca ggatggagaa agttacaaga 900

acccagggaa accagatgga gttaactaca tccgcactga cgaggagggc 950

gacttcagac acaagtcatc gtttgtgatc tgagacccgc ggtgtggctg 1000

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agcagcgcat cccggcggga acccagaaaa ggcttcttac acagcagcct 1450

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tattttgatt attgaaaaga aaatttctat ttaaactgta aatatattgt 1800

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ttttacccaa ggaatcctct catggaagtt tactgtgatg ttccttttct 1950

cacacaagtt ttagcctttt tcacaaggga actcatactg tctacacatc 2000

agaccatagt tgcttaggaa acctttaaaa attccagtta agcaatgttg 2050

aaatcagttt gcatctcttc aaaagaaacc tctcaggtta gctttgaact 2100

gcctcttcct gagatgacta ggacagtctg tacccagagg ccacccagaa 2150

gccctcagat gtacatacac agatgccagt cagctcctgg ggttgcgcca 2200

ggcgcccccg ctctagctca ctgttgcctc gctgtctgcc aggaggccct 2250

gccatccttg ggccctggca gtggctgtgt cccagtgagc tttactcacg 2300
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22

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tgaaacgcct gaatcaaaag cagttttcta attttgactt taaatttttc 2750

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gtagctgcct ataactgaga ctagacggaa aaggaatact cgtgtatttt 3400

aagatatgaa tgtgactcaa gactcgaggc cgatacgagg ctgtgattct 3450

gcctttggat ggatgttgct gtacacagat gctacagact tgtactaaca 3500

caccgtaatt tggcatttgt ttaacctcat ttataaaagc ttcaaaaaaa 3550

ccca 3554

<210> 20
<211> 310
<212> PRT
<213> Homo sapiens

<400> 20

23

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Met Ala Leu Arg Arg Pro Pro Arg Leu Arg Leu Cys Ala Arg Leu
 1               5               10                      15

Pro Asp Phe Phe Leu Leu Leu Leu Phe Arg Gly Cys Leu Ile Gly
                20              25                      30

Ala Val Asn Leu Lys Ser Ser Asn Arg Thr Pro Val Val Gln Glu
                35              40                      45

Phe Glu Ser Val Glu Leu Ser Cys Ile Ile Thr Asp Ser Gln Thr
                50              55                      60

Ser Asp Pro Arg Ile Glu Trp Lys Lys Ile Gln Asp Glu Gln Thr
                65              70                      75

Thr Tyr Val Phe Phe Asp Asn Lys Ile Gln Gly Asp Leu Ala Gly
                80              85                      90

Arg Ala Glu Ile Leu Gly Lys Thr Ser Leu Lys Ile Trp Asn Val
                95              100                     105

Thr Arg Arg Asp Ser Ala Leu Tyr Arg Cys Glu Val Val Ala Arg
                110             115                     120

Asn Asp Arg Lys Glu Ile Asp Glu Ile Val Ile Glu Leu Thr Val
                125             130                     135

Gln Val Lys Pro Val Thr Pro Val Cys Arg Val Pro Lys Ala Val
                140             145                     150

Pro Val Gly Lys Met Ala Thr Leu His Cys Gln Glu Ser Glu Gly
                155             160                     165

His Pro Arg Pro His Tyr Ser Trp Tyr Arg Asn Asp Val Pro Leu
                170             175                     180

Pro Thr Asp Ser Arg Ala Asn Pro Arg Phe Arg Asn Ser Ser Phe
                185             190                     195

His Leu Asn Ser Glu Thr Gly Thr Leu Val Phe Thr Ala Val His
                200             205                     210

Lys Asp Asp Ser Gly Gln Tyr Tyr Cys Ile Ala Ser Asn Asp Ala
                215             220                     225

Gly Ser Ala Arg Cys Glu Glu Gln Glu Met Glu Val Tyr Asp Leu
                230             235                     240

Asn Ile Gly Gly Ile Ile Gly Gly Val Leu Val Val Leu Ala Val
                245             250                     255

Leu Ala Leu Ile Thr Leu Gly Ile Cys Cys Ala Tyr Arg Arg Gly
                260             265                     270

Tyr Phe Ile Asn Asn Lys Gln Asp Gly Glu Ser Tyr Lys Asn Pro
                275             280                     285

Gly Lys Pro Asp Gly Val Asn Tyr Ile Arg Thr Asp Glu Glu Gly
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24

290   295   300
    Asp Phe Arg His Lys Ser Ser Phe Val Ile
                         305   310

<210> 21
<211> 3437
<212> DNA
<213> Homo sapiens

<400> 21
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 gagccgacga cagcgagttc caggcgctgc tggacatctg gtttccggag 150

 gagaagccac tgcccaccgc cttcctggtg gacacatcgg aggaggcgct 200

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 gcctggtgga cgccgccctg caggacctgg agccgcagca gctgctgctg 300

 ttcgtgcagt cgtttggcat ccccgtgtcc agcatgagca aactcctcca 350

 gttcctggac caggcagtgg cccacgaccc ccagactctg gagcagaaca 400

 tcatggacaa gaattacatg gcccacctgg tggaggtcca gcatgagcgc 450

 ggcgcctccg gaggccagac tttccactcc ttgctcacag cctccctgcc 500

 gccccgccga gacagcacag aggcacccaa accaaagagc agcccagagc 550

 agcccatagg ccagggccgg attcgggtgg ggacccagct ccgggtgctg 600

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 cccggaccct cggtggcaga gctccagtcc ccgccccgtg gccctcgccc 700

 tgcagcaggc cctgggccag gagctggccc gcgtcgtcca gggcagcccc 750

 gaggtgccgg gcatcacggt gcgtgtcctg caggccctcg ccaccctgct 800

 cagctcccca cacggcggtg ccctggtgat gtccatgcac cgtagccact 850

 tcctggcctg cccgctgctg cgccagctct gccagtacca gcgctgtgtg 900

 ccacaggaca ccggcttctc ctcgctcttc ctgaaggtgc tcctgcagat 950

 gctgcagtgg ctggacagcc ctggcgtgga gggcgggccc ctgcgggcac 1000

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 gtgcgagggg ggctcctgcg cctggccgag gccctggcct tccgtcagga 1100

 cctggaggtg gtcagctcca ccgtccgtgc cgtcatcgcc accctgaggt 1150

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ttgtggtggt gagctccctg ctgctgcagg aggaggagcc cctggctggg 1350

gggaagccgg gtgcggacgg tggcagcctg gaggccgtgc ggctggggcc 1400

ctcgtcaggc ctcctagtgg actggctgga aatgctggac cccgaggtgg 1450

tcagcagctg ccccgacctg cagctcaggc tgctcttctc ccggaggaag 1500

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catggcctgc cggaagctgg cggtggcgca cccgctgctg ctgctcaggc 2200

acctgcccat gatcgcggcg ctcctgcacg gccgcaccca cctcaacttc 2250

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gaccgaccga ggcctggacg aagagggcga ggaggagagc tcagccggct 2650
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26

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ccttgcccct ggtcagcgtc tccctgttca cccctctgac cgcggccgag 2700

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<210> 22
<211> 1029
<212> PRT
<213> Homo sapiens

<400> 22

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Gly Pro Pro Arg Ala Asp Asp Ser Glu Phe Gln Ala Leu Leu Asp
                20              25                  30

Ile Trp Phe Pro Glu Glu Lys Pro Leu Pro Thr Ala Phe Leu Val
                35              40                  45

Asp Thr Ser Glu Glu Ala Leu Leu Leu Pro Asp Trp Leu Lys Leu
                50              55                  60

Arg Met Ile Arg Ser Glu Val Leu Arg Leu Val Asp Ala Ala Leu
                65              70                  75

Gln Asp Leu Glu Pro Gln Gln Leu Leu Leu Phe Val Gln Ser Phe
                80              85                  90

Gly Ile Pro Val Ser Ser Met Ser Lys Leu Leu Gln Phe Leu Asp
                95              100                 105
```

27

```
Gln Ala Val Ala His Asp Pro Gln Thr Leu Glu Gln Asn Ile Met
              110              115              120

Asp Lys Asn Tyr Met Ala His Leu Val Glu Val Gln His Glu Arg
              125              130              135

Gly Ala Ser Gly Gly Gln Thr Phe His Ser Leu Leu Thr Ala Ser
              140              145              150

Leu Pro Pro Arg Arg Asp Ser Thr Glu Ala Pro Lys Pro Lys Ser
              155              160              165

Ser Pro Glu Gln Pro Ile Gly Gln Gly Arg Ile Arg Val Gly Thr
              170              175              180

Gln Leu Arg Val Leu Gly Pro Glu Asp Asp Leu Ala Gly Met Phe
              185              190              195

Leu Gln Ile Phe Pro Leu Ser Pro Asp Pro Arg Trp Gln Ser Ser
              200              205              210

Ser Pro Arg Pro Val Ala Leu Ala Leu Gln Gln Ala Leu Gly Gln
              215              220              225

Glu Leu Ala Arg Val Val Gln Gly Ser Pro Glu Val Pro Gly Ile
              230              235              240

Thr Val Arg Val Leu Gln Ala Leu Ala Thr Leu Leu Ser Ser Pro
              245              250              255

His Gly Gly Ala Leu Val Met Ser Met His Arg Ser His Phe Leu
              260              265              270

Ala Cys Pro Leu Leu Arg Gln Leu Cys Gln Tyr Gln Arg Cys Val
              275              280              285

Pro Gln Asp Thr Gly Phe Ser Ser Leu Phe Leu Lys Val Leu Leu
              290              295              300

Gln Met Leu Gln Trp Leu Asp Ser Pro Gly Val Glu Gly Gly Pro
              305              310              315

Leu Arg Ala Gln Leu Arg Met Leu Ala Ser Gln Ala Ser Ala Gly
              320              325              330

Arg Arg Leu Ser Asp Val Arg Gly Gly Leu Leu Arg Leu Ala Glu
              335              340              345

Ala Leu Ala Phe Arg Gln Asp Leu Glu Val Val Ser Ser Thr Val
              350              355              360

Arg Ala Val Ile Ala Thr Leu Arg Ser Gly Glu Gln Cys Ser Val
              365              370              375

Glu Pro Asp Leu Ile Ser Lys Val Leu Gln Gly Leu Ile Glu Val
              380              385              390

Arg Ser Pro His Leu Glu Glu Leu Leu Thr Ala Phe Phe Ser Ala
```

28

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                   395                      400                      405
    Thr Ala Asp Ala Ala Ser Pro Phe Pro Ala Cys Lys Pro Val Val
                   410                      415                      420

    Val Val Ser Ser Leu Leu Leu Gln Glu Glu Glu Pro Leu Ala Gly
                   425                      430                      435

    Gly Lys Pro Gly Ala Asp Gly Gly Ser Leu Glu Ala Val Arg Leu
                   440                      445                      450

    Gly Pro Ser Ser Gly Leu Leu Val Asp Trp Leu Glu Met Leu Asp
                   455                      460                      465

    Pro Glu Val Val Ser Ser Cys Pro Asp Leu Gln Leu Arg Leu Leu
                   470                      475                      480

    Phe Ser Arg Arg Lys Gly Lys Gly Gln Ala Gln Val Pro Ser Phe
                   485                      490                      495

    Arg Pro Tyr Leu Leu Thr Leu Phe Thr His Gln Ser Ser Trp Pro
                   500                      505                      510

    Thr Leu His Gln Cys Ile Arg Val Leu Leu Gly Lys Ser Arg Glu
                   515                      520                      525

    Gln Arg Phe Asp Pro Ser Ala Ser Leu Asp Phe Leu Trp Ala Cys
                   530                      535                      540

    Ile His Val Pro Arg Ile Trp Gln Gly Arg Asp Gln Arg Thr Pro
                   545                      550                      555

    Gln Lys Arg Arg Glu Glu Leu Val Leu Arg Val Gln Gly Pro Glu
                   560                      565                      570

    Leu Ile Ser Leu Val Glu Leu Ile Leu Ala Glu Ala Glu Thr Arg
                   575                      580                      585

    Ser Gln Asp Gly Asp Thr Ala Ala Cys Ser Leu Ile Gln Ala Arg
                   590                      595                      600

    Leu Pro Leu Leu Leu Ser Cys Cys Cys Gly Asp Asp Glu Ser Val
                   605                      610                      615

    Arg Lys Val Thr Glu His Leu Ser Gly Cys Ile Gln Gln Trp Gly
                   620                      625                      630

    Asp Ser Val Leu Gly Arg Arg Cys Arg Asp Leu Leu Leu Gln Leu
                   635                      640                      645

    Tyr Leu Gln Arg Pro Glu Leu Arg Val Pro Val Pro Glu Val Leu
                   650                      655                      660

    Leu His Ser Glu Gly Ala Ala Ser Ser Ser Val Cys Lys Leu Asp
                   665                      670                      675

    Gly Leu Ile His Arg Phe Ile Thr Leu Leu Ala Asp Thr Ser Asp
                   680                      685                      690
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29

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Ser Arg Ala Leu Glu Asn Arg Gly Ala Asp Ala Ser Met Ala Cys
            695                 700                 705

Arg Lys Leu Ala Val Ala His Pro Leu Leu Leu Leu Arg His Leu
            710                 715                 720

Pro Met Ile Ala Ala Leu Leu His Gly Arg Thr His Leu Asn Phe
            725                 730                 735

Gln Glu Phe Arg Gln Gln Asn His Leu Ser Cys Phe Leu His Val
            740                 745                 750

Leu Gly Leu Leu Glu Leu Leu Gln Pro His Val Phe Arg Ser Glu
            755                 760                 765

His Gln Gly Ala Leu Trp Asp Cys Leu Leu Ser Phe Ile Arg Leu
            770                 775                 780

Leu Leu Asn Tyr Arg Lys Ser Ser Arg His Leu Ala Ala Phe Ile
            785                 790                 795

Asn Lys Phe Val Gln Phe Ile His Lys Tyr Ile Thr Tyr Asn Ala
            800                 805                 810

Pro Ala Ala Ile Ser Phe Leu Gln Lys His Ala Asp Pro Leu His
            815                 820                 825

Asp Leu Ser Phe Asp Asn Ser Asp Leu Val Met Leu Lys Ser Leu
            830                 835                 840

Leu Ala Gly Leu Ser Leu Pro Ser Arg Asp Asp Arg Thr Asp Arg
            845                 850                 855

Gly Leu Asp Glu Glu Gly Glu Glu Glu Ser Ser Ala Gly Ser Leu
            860                 865                 870

Pro Leu Val Ser Val Ser Leu Phe Thr Pro Leu Thr Ala Ala Glu
            875                 880                 885

Met Ala Pro Tyr Met Lys Arg Leu Ser Arg Gly Gln Thr Val Glu
            890                 895                 900

Asp Leu Leu Glu Val Leu Ser Asp Ile Asp Glu Met Ser Arg Arg
            905                 910                 915

Arg Pro Glu Ile Leu Ser Phe Phe Ser Thr Asn Leu Gln Arg Leu
            920                 925                 930

Met Ser Ser Ala Glu Glu Cys Cys Arg Asn Leu Ala Phe Ser Leu
            935                 940                 945

Ala Leu Arg Ser Met Gln Asn Ser Pro Ser Ile Ala Ala Ala Phe
            950                 955                 960

Leu Pro Thr Phe Met Tyr Cys Leu Gly Ser Gln Asp Phe Glu Val
            965                 970                 975

Val Gln Thr Ala Leu Arg Asn Leu Pro Glu Tyr Ala Leu Leu Cys
```

30

Gln Glu His Ala Ala Val Leu Leu His Arg Ala Phe Leu Val Gly
                     995   1000   1005

Met Tyr Gly Gln Met Asp Pro Ser Ala Gln Ile Ser Glu Ala Leu
                     1010   1015   1020

Arg Ile Leu His Met Glu Ala Val Met
                     1025

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<211> 2186
<212> DNA
<213> Homo sapiens

<400> 23
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  atgaggctcc gcaatggcac cttcctgacg ctgctgctct tctgcctgtg 100

  cgccttcctc tcgctgtcct ggtacgcggc actcagcggc cagaaaggcg 150

  acgttgtgga cgtttaccag cgggagttcc tggcgctgcg cgatcggttg 200

  cacgcagctg agcaggagag cctcaagcgc tccaaggagc tcaacctggt 250

  gctggacgag atcaagaggg ccgtgtcaga aaggcaggcg ctgcgagacg 300

  gagacggcaa tcgcacctgg ggccgcctaa cagaggaccc ccgattgaag 350

  ccgtggaacg gctcacaccg gcacgtgctg cacctgccca ccgtcttcca 400

  tcacctgcca cacctgctgg ccaaggagag cagtctgcag cccgcggtgc 450

  gcgtgggcca gggccgcacc ggagtgtcgg tggtgatggg catcccgagc 500

  gtgcggcgcg aggtgcactc gtacctgact gacactctgc actcgctcat 550

  ctccgagctg agcccgcagg agaaggagga ctcggtcatc gtggtgctga 600

  tcgccgagac tgactcacag tacacttcgg cagtgacaga gaacatcaag 650

  gccttgttcc ccacggagat ccattctggg ctcctggagg tcatctcacc 700

  ctccccccac ttctaccctg acttctcccg cctccgagag tcctttgggg 750

  accccaagga gagagtcagg tggaggacca aacagaacct cgattactgc 800

  ttcctcatga tgtacgcgca gtccaaaggc atctactacg tgcagctgga 850

  ggatgacatc gtggccaagc ccaactacct gagcaccatg aagaactttg 900

  cactgcagca gccttcagag gactggatga tcctggagtt ctcccagctg 950

  ggcttcattg gtaagatgtt caagtcgctg gacctgagcc tgattgtaga 1000

  gttcattctc atgttctacc gggacaagcc catcgactgg ctcctggacc 1050

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atattctgtg ggtgaaagtc tgcaaccccg agaaggatgc gaagcactgt 1100

gaccggcaga aagccaacct gcggatccgc ttcaaaccgt ccctcttcca 1150

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acaaagactt tggaaagcag gcgctgcgga aggagcatgt gaacccgcca 1250

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caggcggccc ccacactgtg cctgaggccc ggaaccgttc gcacccggcc 1950

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attcttggat acatttgatt ttttcacgta agtccacata tacttctata 2100

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<211> 548
<212> PRT
<213> Homo sapiens

<400> 24
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1               5                   10                  15

Leu Cys Ala Phe Leu Ser Leu Ser Trp Tyr Ala Ala Leu Ser Gly
                20                  25                  30
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32

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Gln Lys Gly Asp Val Val Asp Val Tyr Gln Arg Glu Phe Leu Ala
                35              40                  45

Leu Arg Asp Arg Leu His Ala Ala Glu Gln Glu Ser Leu Lys Arg
                50              55                  60

Ser Lys Glu Leu Asn Leu Val Leu Asp Glu Ile Lys Arg Ala Val
                65              70                  75

Ser Glu Arg Gln Ala Leu Arg Asp Gly Asp Gly Asn Arg Thr Trp
                80              85                  90

Gly Arg Leu Thr Glu Asp Pro Arg Leu Lys Pro Trp Asn Gly Ser
                95              100                 105

His Arg His Val Leu His Leu Pro Thr Val Phe His His Leu Pro
                110             115                 120

His Leu Leu Ala Lys Glu Ser Ser Leu Gln Pro Ala Val Arg Val
                125             130                 135

Gly Gln Gly Arg Thr Gly Val Ser Val Val Met Gly Ile Pro Ser
                140             145                 150

Val Arg Arg Glu Val His Ser Tyr Leu Thr Asp Thr Leu His Ser
                155             160                 165

Leu Ile Ser Glu Leu Ser Pro Gln Glu Lys Glu Asp Ser Val Ile
                170             175                 180

Val Val Leu Ile Ala Glu Thr Asp Ser Gln Tyr Thr Ser Ala Val
                185             190                 195

Thr Glu Asn Ile Lys Ala Leu Phe Pro Thr Glu Ile His Ser Gly
                200             205                 210

Leu Leu Glu Val Ile Ser Pro Ser Pro His Phe Tyr Pro Asp Phe
                215             220                 225

Ser Arg Leu Arg Glu Ser Phe Gly Asp Pro Lys Glu Arg Val Arg
                230             235                 240

Trp Arg Thr Lys Gln Asn Leu Asp Tyr Cys Phe Leu Met Met Tyr
                245             250                 255

Ala Gln Ser Lys Gly Ile Tyr Tyr Val Gln Leu Glu Asp Asp Ile
                260             265                 270

Val Ala Lys Pro Asn Tyr Leu Ser Thr Met Lys Asn Phe Ala Leu
                275             280                 285

Gln Gln Pro Ser Glu Asp Trp Met Ile Leu Glu Phe Ser Gln Leu
                290             295                 300

Gly Phe Ile Gly Lys Met Phe Lys Ser Leu Asp Leu Ser Leu Ile
                305             310                 315

Val Glu Phe Ile Leu Met Phe Tyr Arg Asp Lys Pro Ile Asp Trp
```

33

```
                320                    325                    330

    Leu Leu Asp His Ile Leu Trp Val Lys Val Cys Asn Pro Glu Lys
                335                    340                    345

    Asp Ala Lys His Cys Asp Arg Gln Lys Ala Asn Leu Arg Ile Arg
                350                    355                    360

    Phe Lys Pro Ser Leu Phe Gln His Val Gly Thr His Ser Ser Leu
                365                    370                    375

    Ala Gly Lys Ile Gln Lys Leu Lys Asp Lys Asp Phe Gly Lys Gln
                380                    385                    390

    Ala Leu Arg Lys Glu His Val Asn Pro Pro Ala Glu Val Ser Thr
                395                    400                    405

    Ser Leu Lys Thr Tyr Gln His Phe Thr Leu Glu Lys Ala Tyr Leu
                410                    415                    420

    Arg Glu Asp Phe Phe Trp Ala Phe Thr Pro Ala Ala Gly Asp Phe
                425                    430                    435

    Ile Arg Phe Arg Phe Phe Gln Pro Leu Arg Leu Glu Arg Phe Phe
                440                    445                    450

    Phe Arg Ser Gly Asn Ile Glu His Pro Glu Asp Lys Leu Phe Asn
                455                    460                    465

    Thr Ser Val Glu Val Leu Pro Phe Asp Asn Pro Gln Ser Asp Lys
                470                    475                    480

    Glu Ala Leu Gln Glu Gly Arg Thr Ala Thr Leu Arg Tyr Pro Arg
                485                    490                    495

    Ser Pro Asp Gly Tyr Leu Gln Ile Gly Ser Phe Tyr Lys Gly Val
                500                    505                    510

    Ala Glu Gly Glu Val Asp Pro Ala Phe Gly Pro Leu Glu Ala Leu
                515                    520                    525

    Arg Leu Ser Ile Gln Thr Asp Ser Pro Val Trp Val Ile Leu Ser
                530                    535                    540

    Glu Ile Phe Leu Lys Lys Ala Asp
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<210> 25
<211> 43
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 25
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34

<210> 26
<211> 41
<212> DNA
<213> Artificial Sequence

<220>
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<210> 27
<211> 19
<212> DNA
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<220>
<223> Synthetic Oligonucleotide Probe

<400> 27
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<210> 28
<211> 23
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<220>
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<400> 28
 aggcctttac ccaaggccac aac 23

<210> 29
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<220>
<223> Synthetic Oligonucleotide Probe

<400> 29
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<210> 30
<211> 22
<212> DNA
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<220>
<223> Synthetic Oligonucleotide Probe

<400> 30
 tcccaccact tacttccatg aa 22

<210> 31
<211> 25
<212> DNA

35

<213> Artificial Sequence

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<223> Synthetic Oligonucleotide Probe

<400> 31
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<210> 32
<211> 23
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<220>
<223> Synthetic Oligonucleotide Probe

<400> 32
attgtcctga gattcgagca aga 23

<210> 33
<211> 18
<212> DNA
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<220>
<223> Synthetic Oligonucleotide Probe

<400> 33
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<210> 34
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<400> 34
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<210> 35
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<400> 35
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<210> 36
<211> 19
<212> DNA
<213> Artificial Sequence

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<223> Synthetic Oligonucleotide Probe

<400> 36
ccagtcaggc cgttttaga 19

<210> 37
<211> 21
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<220>
<223> Synthetic Oligonucleotide Probe

<400> 37
cgggcgccca agtaaaagct c 21

<210> 38
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<212> DNA
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<220>
<223> Synthetic Oligonucleotide Probe

<400> 38
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